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## RAW SEQUENCE LISTING

DATE: 04/30/2002

PATENT APPLICATION: US/09/928,522

TIME: 14:07:11

Input Set : N:\Crif3\RULE60\09928522.raw

Output Set: N:\CRF3\04302002\I928522.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Spurlock, Michael E.

7 (ii) TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID

8 SEQUENCES CODING THEREFOR AND USES THEREOF

10 (iii) NUMBER OF SEQUENCES: 8

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.

14 (B) STREET: Suite 2100 111 East Wisconsin Avenue

15 (C) CITY: Milwaukee

16 (D) STATE: Wisconsin

17 (E) COUNTRY: USA

18 (F) ZIP: 53202

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/928,522

C--> 28 (B) FILING DATE: 13-Aug-2001

29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/08/688,908

33 (B) FILING DATE: 31-JUL-1996

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Plotecher, Gary R.

38 (B) REGISTRATION NUMBER: 27,830

39 (C) REFERENCE/DOCKET NUMBER: PM-8808

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 414-273-2100

43 (B) TELEFAX: 414-223-5000

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 36 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

54 (ii) MOLECULE TYPE: other nucleic acid

55 (A) DESCRIPTION: /desc = "Primer"

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 GGATCCGGTC TCAGGCCGTG CCYATCCARA AAGTCC

64 (2) INFORMATION FOR SEQ ID NO: 2:

ENTERED

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66      (i) SEQUENCE CHARACTERISTICS:
67          (A) LENGTH: 30 base pairs
68          (B) TYPE: nucleic acid
69          (C) STRANDEDNESS: single
70          (D) TOPOLOGY: linear
72      (ii) MOLECULE TYPE: other nucleic acid
73          (A) DESCRIPTION: /desc = "Primer"
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
80 GAATTCAGCG CTGCAYYCAG GGCTRASRTC                                     30
82 (2) INFORMATION FOR SEQ ID NO: 3:
84      (i) SEQUENCE CHARACTERISTICS:
85          (A) LENGTH: 449 base pairs
86          (B) TYPE: nucleic acid
87          (C) STRANDEDNESS: single
88          (D) TOPOLOGY: linear
90      (ii) MOLECULE TYPE: cDNA
93      (ix) FEATURE:
94          (A) NAME/KEY: CDS
95          (B) LOCATION: 6..443
98      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
100 AGGCC GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA ACC CTC ATC         47
101     Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile
102         1             5             10
104 AAG ACA ATT GTC ACC AGG ATC AAT GAC ATC TCA CAC ACG CAG TCC GTC         95
105 Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val
106 15             20             25             30
108 TCC TCC AAA CAG AGG GTC ACT GGT TTG GAC TTC ATC CCT GGG CTC CAC        143
109 Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His
110             35             40             45
112 CCT CTC CTG AGT TTG TCC AAG ATG GAC CAG ACA TTG GCG ATC TAC CAA        191
113 Pro Leu Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln
114             50             55             60
116 CAG ATC CTC ACC AGT CTG CCT TCC AGA AAT GTG GTC CAA ATA TCC AAT        239
117 Gln Ile Leu Thr Ser Leu Pro Ser Arg Asn Val Val Gln Ile Ser Asn
118             65             70             75
120 GAC CTG GAG AAC CTC CGG GAC CTT CTC CAC CTG CTG GCC GCC TCC AAG        287
121 Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ala Ser Lys
122             80             85             90
124 AGC TGC CCC TTG CCG CAG GTC AGG GCC CTG GAG AGC TTG GAG AGC TTG        335
125 Ser Cys Pro Leu Pro Gln Val Arg Ala Leu Glu Ser Leu Glu Ser Leu
126 95             100             105             110
128 GGT GTC GTC CTG GAA GCC TCC CTC TAC TCC ACC GAG GTG GTG GCC CTG        383
129 Gly Val Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu
130             115             120             125
132 AGC CGG CTG CAG GGG TCA CTA CAG GAC ATG TTG CGG CAG CTG GAC CTC        431
133 Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Arg Gln Leu Asp Leu
134             130             135             140
136 AGC CCT GAA TGC AGCGCT                                         449
137 Ser Pro Glu Cys

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138 145

141 (2) INFORMATION FOR SEQ ID NO: 4:

143 (i) SEQUENCE CHARACTERISTICS:

144 (A) LENGTH: 146 amino acids

145 (B) TYPE: amino acid

146 (D) TOPOLOGY: linear

148 (ii) MOLECULE TYPE: protein

150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

152 Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr

153 1 5 10 15

155 Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser

156 20 25 30

158 Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Leu

159 35 40 45

161 Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile

162 50 55 60

164 Leu Thr Ser Leu Pro Ser Arg Asn Val Val Gln Ile Ser Asn Asp Leu

165 65 70 75 80

167 Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ala Ser Lys Ser Cys

168 85 90 95

170 Pro Leu Pro Gln Val Arg Ala Leu Glu Ser Leu Glu Ser Leu Gly Val

171 100 105 110

173 Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg

174 115 120 125

176 Leu Gln Gly Ser Leu Gln Asp Met Leu Arg Gln Leu Asp Leu Ser Pro

177 130 135 140

179 Glu Cys

180 145

182 (2) INFORMATION FOR SEQ ID NO: 5:

184 (i) SEQUENCE CHARACTERISTICS:

185 (A) LENGTH: 445 base pairs

186 (B) TYPE: nucleic acid

187 (C) STRANDEDNESS: single

188 (D) TOPOLOGY: linear

190 (ii) MOLECULE TYPE: cDNA

195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

197 AAGCTGTGCC CATCAAAAA GTCCAAGATG ACACCAAAAC CCTCATCAAG ACAATTGTCA 60

199 CCAGGATCAA TGACATTTCA CACACGCAGT CAGTCTCCTC CAAACAGAAA GTCACCGGTT 120

201 TGGACTTCAT TCCTGGGCTC CACCCCATCC TGACCTTATC CAAGATGGAC CAGACACTGG 180

203 CAGTCTACCA ACAGATCCTC ACCAGTATGC CTTCCAGAAA CGTGATCCAA ATATCCAACG 240

205 ACCTGGAGAA CCTCCGGGAT CTTCTTCACG TGCTGGCCTT CTCTAAGAGC TGCCACTTGC 300

207 CCTGGGCCAG TGGCCTGGAG ACCTTGGACA GCCTGGGGGG TGTCCTGGAA GCTTCAGGCT 360

209 ACTCCACAGA GGTGGTGGCC CTGAGCAGGC TGCAGGGGTC TCTGCAGGAC ATGCTGTGGC 420

211 AGCTGGACCT CAGCCCTGGG TGCTG 445

213 (2) INFORMATION FOR SEQ ID NO: 6:

215 (i) SEQUENCE CHARACTERISTICS:

216 (A) LENGTH: 445 base pairs

217 (B) TYPE: nucleic acid

218 (C) STRANDEDNESS: single

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219         (D) TOPOLOGY: linear
221     (ii) MOLECULE TYPE: cDNA
226     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
228 AAGCAGTGCC TATCCAGAAA GTCCAGGATG ACACCAAAAC CCTCATCAAG ACCATTGTCA      60
230 CCAGGATCAA TGACATTTC CACACGCAGT CGGTATCCGC CAAGCAGAGG GTCCTGGCT      120
232 TGGACTTCAT TCCTGGGCTT CACCCCATTC TGAGTTGTG CAAGATGGAC CAGACTCTGG      180
234 CAGTCTATCA ACAGGTCCTC ACCAGCCTGC CTTCCCAAAA TGTGCTGCAG ATAGCCAATG      240
236 ACCTGGAGAA TCTCCGAGAC CTCCTCCATC TGCTGGCCTT CTCCAAGAGC TGCTCCCTGC      300
238 CTCAGACCAG TGGCCTGCAG AAGCCAGAGA GCCTGGATGG CGTCCTGGAA GCCTCACTCT      360
240 ACTCCACAGA GGTGGTGGCT TTGAGCAGGC TGCAGGGCTC TCTGCAGGAC ATTCTTCAAC      420
242 AGTTGGATGT TAGCCCTGAA TGCTG                                     445
244 (2) INFORMATION FOR SEQ ID NO: 7:
246     (i) SEQUENCE CHARACTERISTICS:
247         (A) LENGTH: 167 amino acids
248         (B) TYPE: amino acid
249         (C) STRANDEDNESS:
250         (D) TOPOLOGY: linear
252     (ii) MOLECULE TYPE: protein
257     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
259 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
260 1          5          10          15
262 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
263          20          25          30
265 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
266          35          40          45
268 Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
269          50          55          60
271 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
272          65          70          75          80
274 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
275          85          90          95
277 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
278          100         105         110
280 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
281          115         120         125
283 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
284          130         135         140
286 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
287          145         150         155         160
289 Leu Asp Leu Ser Pro Gly Cys
290          165
292 (2) INFORMATION FOR SEQ ID NO: 8:
294     (i) SEQUENCE CHARACTERISTICS:
295         (A) LENGTH: 167 amino acids
296         (B) TYPE: amino acid
297         (C) STRANDEDNESS:
298         (D) TOPOLOGY: linear
300     (ii) MOLECULE TYPE: protein
305     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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307 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
308 1 5 10 15
310 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
311 20 25 30
313 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
314 35 40 45
316 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
317 50 55 60
319 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
320 65 70 75 80
322 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
323 85 90 95
325 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
326 100 105 110
328 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
329 115 120 125
331 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
332 130 135 140
334 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
335 145 150 155 160
337 Leu Asp Val Ser Pro Glu Cys
338 165

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/928,522

DATE: 04/30/2002

TIME: 14:07:12

Input Set : N:\Crf3\RULE60\09928522.raw

Output Set: N:\CRF3\04302002\I928522.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]